Single timepoint models of dynamic systems.

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Public Summary:

Many interesting studies aimed at elucidating the connectivity structure of biomolecular pathways make use of abundance measurements, and employ statistical and information theoretic approaches to assess connectivities. These studies often do not address the effects of the dynamics of the underlying biological system, yet dynamics give rise to impactful issues such as timepoint selection and its effect on structure recovery. In this work, we study conditions for reliable retrieval of the connectivity structure of a dynamic system, and the impact of dynamics on structure-learning efforts. We encounter an unexpected problem not previously described in elucidating connectivity structure from dynamic systems, show how this confounds structure learning of the system and discuss possible approaches to overcome the confounding effect. Finally, we test our hypotheses on an accurate dynamic model of the IGF signalling pathway. We use two structure-learning methods at four time points to contrast the performance and robustness of those methods in terms of recovering correct connectivity.

Scientific Abstract:

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